Claims

[c1] 1.A method for detecting the binding of a plurality of proteins with a plurality of nucleic acids comprising:

a.obtaining a plurality of candidate fragments from the nucleic acids; wherein the candidate fragments contain binding sites for the proteins and wherein the plurality of proteins have at least 50 proteins; and

b. detecting the candidate fragments.

[c2] 2. The method of claim 1, wherein the nucleic acid is DNA.

[c3] 3.The method of Claim 2 wherein the nucleic acid is genomic DNA.

[c4] 4.The method of Claim 3 wherein the candidate fragments are obtained by DNA foot printing.

[c5] 5.The method of Claim 4 wherein the step of determining candidate fragments comprises hybridizing the candidate fragments with a collection of nucleic acid probes.

[c6] 6.The method of Claim 5 wherein the nucleic acid probes are immobilized on a collection of beads or optical fibers.

[c7] 7.The method of Claim 5 wherein the nucleic acid probes are immobilized on a substrate.

[c8] 8.The method of Claim 7 wherein the collection of nucleic acid probes contain at least 10,000 probes.

[c9] 9.The method of Claim 8 wherein the collection of nucleic acid probes contain at least 50,000 probes.

[c10] 10.The method of Claim 9 wherein the collection of nucleic acid probes contain at least 100,000 probes.

[c11] 11.The method of Claim 10 wherein the collection of nucleic acid probes contain at least 1,000,000 probes.

[c12] 12.The method of Claim 10 wherein the nucleic acid probes are oligonucleotide

probes.

[c13] 13.The method of Claim 12 wherein the oligonucleotide probes are between 10-50 in length.

[c14] 14.The method of Claim 13 wherein the oligonucleotide probes tile genomic sequences of interest.

[c15] 15.The method of Claim 14 wherein the genomic sequences of interest contain genic regions.

[c16] 16.The method of claim 14, where the forward and lower strand sequences are tiled.

[c17] 17.The method of Claim 15 wherein at least one of the binding proteins is unknown.

[c18] 18.A method for obtaining a profile of protein binding to the genomic DNA of a biological sample comprising:
a.obtaining a plurality of candidate fragments from genomic DNA by eliminating unbound genomic DNA; and
b.detecting the candidate fragments.

[c19] 19.The method of claim 18, wherein the candidate fragments are obtained by DNA foot printing.

[c20] 20.The method of Claim 19 wherein the step of determining candidate fragments comprises hybridizing the candidate fragments with a collection of nucleic acid probes.

[c21] 21.The method of Claim 20 wherein the nucleic acid probes are immobilized on a collection of beads or optical fibers.

[c22] 22.The method of Claim 20 wherein the nucleic acid probes are immobilized on a substrate.

[c23] 23.The method of Claim 22 wherein the collection of nucleic acid probes contains at least 10,000 probes.

[c24] 24.The method of Claim 23 wherein the collection of nucleic acid probes contains at least 50,000 probes.

[c25] 25.The method of Claim 24 wherein the collection of nucleic acid probes contains at least 100,000 probes.

[c26] 26.The method of Claim 25 wherein the collection of nucleic acid probes contains at least 1,000,000 probes.

[c27] 27.The method of Claim 26 wherein the nucleic acid probes are oligonucleotide probes.

[c28] 28.The method of Claim 27 wherein the oligonucleotide probes are between 10-50 in length.

[c29] 29.The method of Claim 28 wherein the oligonucleotide probes tile genomic sequences of interest.

[c30] 30.The method of Claim 29 wherein the genomic sequences of interest contain genic regions.

[c31] 31.The method of claim 29, where the forward and lower strand sequences are tiled.

[c32] 32.The method of Claim 31 wherein at least one of the binding proteins is unknown.

[c33] 33.A method for analyzing gene expression regulation comprising:
a)obtaining a first set of candidate fragments from the genomic DNA of a first sample, wherein the first sample is a control sample;
b)obtaining a second set candidate fragments from the genomic DNA of a second sample, wherein the second sample is treated; and
c) comparing the first and second sets of candidate fragments.

[c34] 34.The method of claim 33 wherein the candidate fragments are obtained by DNA foot printing.

[c35] 35.The method of Claim 34 wherein the second sample is treated with a

pharmaceutical agent.

[c36] 36.The method of Claim 34 wherein the second sample is treated with environmental change.

[c37] 37.The method of Claim 36 wherein the step of comparing candidate fragments comprises hybridizing the first and second sets of candidate fragments with the same collection of nucleic acid probes.

[c38] 38.The method of Claim 37 wherein the step of comparing candidate fragments comprises hybridizing the first and second sets of candidate fragments with a first and second collections of nucleic acid probes.

[c39] 39.The method of Claim 38 wherein the first and second collection of nucleic acid probes are the same.

[c40] 40.The method of Claim 37, 38 or 39 wherein the nucleic acid probes are immobilized on a collection of beads or optical fibers.

[c41] 41.The method of Claim 37, 38 or 39 wherein the nucleic acid probes are immobilized on a substrate.

[c42] 42.The method of Claim 41 wherein the collection of nucleic acid probes contains at least 10,000 probes.

[c43] 43.The method of Claim 42 wherein the collection of nucleic acid probes contains at least 50,000 probes.

[c44] 44.The method of Claim 43 wherein the collection of nucleic acid probes contains at least 100,000 probes.

[c45] 45.The method of Claim 44 wherein the collection of nucleic acid probes contains at least 1,000,000 probes.

[c46] 46.The method of Claim 42 wherein the nucleic acid probes are oligonucleotide probes.

[c47] 47.The method of Claim 46 wherein the oligonucleotide probes are between 10-50 in length.

[c48] 48.The method of Claim 47 wherein the oligonucleotide probes tile genomic sequences of interest.

[c49] 49.The method of Claim 48 wherein the genomic sequences of interest contain genic regions.

[c50] 50.The method of claim 49 where the forward and lower strand sequences are tiled.

[c51] 51.The method of Claim 50 wherein at least one of the binding proteins is unknown.